

APPENDIX A

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Group Art Unit 1638
Examiner: Anne R. Kubelik

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axmi008	-----GVRGPSHRLS-----NAACVVYGNRSRVNVY	GWTHSTSLKRENIIEANQIT	515
cry1Ca	NS-----VPPREGYSHRLCHATFVQSGT---PFLT	TGVVFSWTHRSATLTNTIDPERIN	468
cry1Aa	NS-----VPPRAGFSHRLSHVTMLSQAAG--AVYT	TLRAPTFWQHRSAEFNIIIPSSQIT	471
cry1Ac	NN-----VPPRQGFHRLSHVSMFRSGFSNSSVSI	IRAPMFSWIHRSAEFNIIIASDSIT	472
cry1Ia	TG-----QPNYESYSHRLSHIGLISASHVK-ALVYS	-----WTHRSADRTNTIEPNSIT	508
cry2Aa	DLTR---PLHYNQIRNIESPSGTPGGARAYLVSVHN	RKNNIYAANENGTMHILAPEDYT	492
cry3Aa1	TD-----EPLEKGYSHQLNVMCFLMQGSR----	GTIPVLTWTHKSVDFNMDSSKIT	518
cry3Bb	TD-----EPLEKAYSHQLNYAECFLMQDRR----	GTIPFFTWTWTHRSVDFNTIDAELIT	513
cry4Aa	NQGNPTLFPTYDNYSHILSFIKLSIPATYKTQV---	YTFAWTHSSVDPKNTIYTHLTT	539
cry4Ba	NQ-----PTVNDYTHILSYIKTDVI--DYN	SNR-----VSFAWTHKIVDPNNQIYDAIT	481
cry6Aa	SN-----QYMSHEYTSLPNNFMLS	RNS	445
cry7Aa	E-----PIHEKYTHRLCHATAIFKSTP--DYD	NATIPISWTHRSAEYNNRIYPNKIT	498
cry8Aa	T-----VPVAESYSHRLSHITSHSFSKNG-SAYY	GSPVFWTHTSADLNNTIYSDKIT	527
cry10Aa	EE-----YGHTLSYIKTDNYIFS	VVRERRR--VAFSWTHTSVDFQNTIDLDNIT	511
cry16Aa	AK-----YNDYNHILSYMLINGETFGQKRHG---	YSFAFTHSSVDPNNTIAANKIT	513
cry19Ba	TT-----YNDYNHILSYMLINGETFGQKRHG---	YSFAFTHSSVDRYNTIVDPKIV	507
cry24Aa	G-----NANDYSHLLCDVKILQEDSSNICEGR	SLLSHAWTHASLDRNNTILPDEIT	516
cry25Aa	HW-----ISDMMTINQSVQLASNPTQTF	AFSALSIGWHHSSAGNRNVYVDKIT	525
cry39Aa1	LT-----YENYSHILSYMTS-AQHFGDKKIG---	YTFAWMHESVDFDNRVDPDKIT	502
cry40Aa1	P-----SYRDYSHRLS-----NAACVGAGN	SRINVYGWTHTSMSKYNLIYPDKIT	513

axmi008	--QIPAVKSYLLQNYLANAYTYVIKGT-HTGGDL	IRFLRTKSEYNAVYAGGGIRLIINN	572
cry1Ca	--QIPLVKGFVWG-----GTSVITGPGFTGGDI	LRNTFG--DFVSLQVNINSPI---	515
cry1Aa	--QIPLTKSTNLGS-----GTSVVKGPGFTGGDI	LRRTSPG--QISTLRVNITAPL---	518
cry1Ac	--QIPAVKGNFLFN-----G-SVISGPGFTGGDL	VRLNSSG--NNIQNRGYIEVPIHFP	521
cry1Ia	--QIPLVKAFNLSS-----GAAVVRGPGFTGGDI	LRRTNTG--TFGDIRVNINPPF---	555
cry2Aa	GFTISPIHATQVNN-----QTRTFISEKFGNQ	GDLSIRFEQSN-----TTARYTLR	537
cry3Aa1	--QLPLVKAYKLS-----GASVVGPRFTGGDI	IQCTENG--SAATYVTP-DVSY-	566
cry3Bb	--QLPVVKAYALSS-----GASIIEGPGFTGGNLI	FLKESSN--SIKFKVTLNSAALL-	563
cry4Aa	--QIPAVKANSLGT-----ASKVVQPGHGTGGDL	IDFKDH-----FKITCQHSNF-	582
cry4Ba	--QVPAVKSNFLNA-----TAKVIKPGHGTGGDL	VALTSNGT--LSGR-MEIQCKTSIFN	531
cry6Aa	-----		
cry7Aa	--KIPAVKMYKLDD-----PSTVVKGPGFTGGDL	VKRGSTG--YIGDIKATVNSPL---	545
cry8Aa	--QIPAVKGDMLYL-----GGSVVQPGFTGGDI	LKRTNPS--ILGTFAVTVNGSL---	574
cry10Aa	--QIHALKALKVSS-----DSKIVKPGHGTGGDL	VILKDS-----MDFRVRFLK	553
cry16Aa	--QIPVVKASSING-----SISIEKPGFTGGDL	VKMRADS-----GLTMRFKAE	556
cry19Ba	--QIPAVKTNLVG-----ANIIKPGHGTGGDLI	KLEYER-----FLSLRIK-L	547
cry24Aa	--QIPAVTAYELR-----GNSSVVGPGSTGGDL	VKMS-----YHSVWSFKVYC	558
cry25Aa	--QIPATKTVREHP-----MIKPGPGFTGGDL	ADLSSNSD--ILQYDLRSYDDRL	571
cry39Aa1	--QIPAVKGDYLQY-----GYVKQPGHGTGGDL	VSMIRTD-----RLGINVY-F	543
cry40Aa1	--QIPAVKAFDIS-----DTGPGQVIAGPGHGT	GGNVVSLP-----YYSRLKIRLIP--A	558

HIGHLIGHTED SEQUENCES = Blocks A-F (de Maagd et al. (1999) *Appl. Environ. Microbiol.* 65:4369-4374)

BLOCKED SEQUENCES = Conserved domains 3-5

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axmi008	TAGQSYRIRFRYAADKAAFFSVLYLPGGWGSN-----RFVSLEKSYSGNYDDLKYSDFK	626
cry1Ca	--TQRYRLRFRYASSRDARVIVLTCAASTGVGGQVSVNMPLQKIMEICE---NLTSRPFER	570
cry1Aa	--SQRYRVIRIRYASTTNLQFHTSIDGRPINQG-----NFSATMSSGS---NLQSGSFR	566
cry1Ac	STSTRYRVIRYASVTPIHLNVNWGNSSIFS-----TVPATATSLD---NLQSSDFG	571
cry1Ia	--AQRYRVIRIRYASTTDLQFHTSINGKAINQG-----NFSATMNRGE---DLDYKTFR	603
cry2Aa	GNGNSYNLYLRVSSIGNSTIRVTINGRVYTVS-----NVNTTTMNDG---VNDNGAR	586
cry3Aa1	---QKYRARIHYASTSQITFTLSLDGAPFNQY-----YFDKTINKGD---TLTYNSFN	613
cry3Bb	---QRYRVIRIRYASTTNLRLFVQNSNNDFLVI-----YINKTMNKDD---DLTYQTFD	610
cry4Aa	--QQSYFIRIRYASNGSANTRAVINLSIPGVAELG-MALNPTFSGTD---YTNLKYKDFQ	636
cry4Ba	DPTRSYGLRIRYAAN--SPIVLNVSYVLQGVSRGTTISTESTFSRPNNIIPDLDKYEEFR	589
cry6Aa	-----NLEYKCPENNFMIIWYNNNSDWYNN-----	469
cry7Aa	--SQKYRVIRYATNVSGQFNVIYINDKITLQT---KFQNTVETIGEGK---DLTYGSFG	596
cry8Aa	--SQRYRVIRIRYASTTDFEFTLYLG-DTIEKN-----RFNKTMDNGA---SLTYETFK	621
cry10Aa	NVSRQYQVIRIRYATNAPKTTVFLTGIDTISVELPSTTSRQNP-----ATDLTYADFG	606
cry16Aa	LLDKKYRVIRIRYKQNYSSKLILRKWKGEYIQQIHNIS--PTYGAFSY-----LE	605
cry19Ba	IASMTFRIRIRYASNISGOMMINIGYQNPTYFNIIPTTS--RDYTELK-----FE	595
cry24Aa	SELKNYRVIRIRYASHGNCQFLMKRWPSTGVAP-----RQWARHNVQGTFSNSMRYEAFK	612
cry25Aa	TEDVPFRIRIRCASIGVSTISVDNWGSSSPQVT-----VASTAASLDT---LKYESFQ	621
cry39Aa1	PQFLDYRIRIRYSTSSNGYLYIYSPNTKIVYLPPTTLVDGQPTFDPM-----FS	593
cry40Aa1	STNKNYLVRVRYTSTSNGRLLVERWSPSSIIN-----SYFFLPSTGPG--DSFGYVDTL	610

axmi008	FAEIIITPPLPSSNIQMDVEMQANSFQS---DVNVLDKIEFLPSNTTTLEYEGERDLEK	682
cry1Ca	YTFDFSNPFSSFRANPDIIIGTSEOPLEFCAGSISSGELYIDKIEIILADATFEA---ESDLER	627
cry1Aa	TVGFTTFFNFSSNGSSVFTLSAHVFN-----SGNEVYIDRIEFVPAEVTFEA---EYDLER	618
cry1Ac	YFESANAFTSSLGN---IVGVNFS-----GTAGVIIDRFEFIPVTATLEA---EYNLER	620
cry1Ia	TVGFTTFFSFLDVQSTFTTIGAWNFS-----SGNEVYIDRIEFVPEVTYEA---EYDFEK	655
cry2Aa	FSDINIGNIVASDNTNVTLNINVTLSN---GTFEDLMNIMFVPTNLPPPLY-----	633
cry3Aa1	LASFSTPFELSG---NNLQIGVTGLS-----AGDKVYIDKIEFIPVN-----	652
cry3Bb	LATTNSNMFGSGDKNELIIGAESFV---SNEKIYIDKIEFIPVQL-----	652
cry4Aa	YLEFSN---EVKFAPNQNISLVFNRS-DVYNTTTLIDKIEFLPITRSIREDREKQKLET	692
cry4Ba	YKDPFDAIVPMRLSSNLITIAIQPLN-MTSNNQVIIDRIEIIPIITQSVLDETENQNLES	648
cry6Aa	-SDWYNN-----	475
cry7Aa	YIEYSTTIQFPDEHPKITLHLSDL-----NNSSFYVDSIEFIPVDVNYAE---KEKLEK	648
cry8Aa	FASFITDFQFRETQDKILLSMGDFS-----SGQEVYIDRIEFIPVDETYEA---EQDLEA	673
cry10Aa	YVTFPRTVPNKTFEGEDTLLMTLYGTP-NHSYN-IYIDKIEFIPITQSVLDYTEKQNIK	664
cry16Aa	SFTITTTENIFDLTMEVTPYGRQFVE-DIPS--LILDKIEFLPTN-----	648
cry19Ba	DFQLVDTSYIYSGGPSISS--NTLWLD-NFSNGHVIIDKIEFIPLGITLNQAQGYDYTDQ	652
cry24Aa	YLDIFTITP-----EENNAFTIDLES---GGDLFIDKIEFIPVSGSAFEYEGKQNIK	663
cry25Aa	YVSIPGNYYFDSAPRIRLLR-----QPGRLLDVRIEIIIPVNFPLS-----EQ	664
cry39Aa1	AFRVVEVPASFR--ASVAG--YTNTTI-EAGFGFVYIDKIEFIPDNTTTLEYEGGRDLEK	648
cry40Aa1	VTFNQP-----GVEIIIQNLDT---PIN--VDKVEFIPVNSTALEYEGKQSLEK	655